Re-run

#8

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/679,643

DATE: 08/03/2004
TIME: 14:09:20

Input Set : **N:\DA\US09679643.raw**
Output Set: **N:\CRF4\08022004\I679643.raw**

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 1 <110> APPLICANT: Foster, Timothy J.
 2         McDevitt, Damien L.
 3 <120> TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
 4 <130> FILE REFERENCE: 05344.105011
 5 <140> CURRENT APPLICATION NUMBER: US/09/679,643
 6 <141> CURRENT FILING DATE: 2000-10-05
 7 <150> PRIOR APPLICATION NUMBER: US/08/293,728
 8 <151> PRIOR FILING DATE: 1994-08-22
 9 <160> NUMBER OF SEQ ID NOS: 20
10 <170> SOFTWARE: PatentIn Ver. 2.0
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13 <211> LENGTH: 3498
14 <212> TYPE: DNA
15 <213> ORGANISM: Staphylococcus aureus
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (301)..(3099)
19 <400> SEQUENCE: 1
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21      ggtagagttc atattaataa taaaaaatgt ttgcaatcaa atcgtacgtt gtcgtttgta 120
22      attcttaaaa tagcaataaa taaaatgttt gttagtaaag tattattgtg gataataaaa 180
23      tatcgataca aattaattgc tataatgcaa ttttagtgta taattccatt aacagagatt 240
24      aaatatatct taagggtat atagttaata taaaatgact ttttaaaaag agggaataaa 300
25      atg aat atg aag aaa aaa gaa aaa cac gca att cgg aaa aaa tcg att 348
26      Met Asn Met Lys Lys Lys Glu Lys His Ala Ile Arg Lys Lys Ser Ile
27       1               5                  10                  15
28      ggc gtg gct tca gtg ctt gta ggt acg tta atc ggt ttt gga cta ctc 396
29      Gly Val Ala Ser Val Leu Val Gly Thr Leu Ile Gly Phe Gly Leu Leu
30                      20                 25                  30
31      agc agt aaa gaa gca gat gca agt gaa aat agt gtt acg caa tct gat 444
32      Ser Ser Lys Glu Ala Asp Ala Ser Glu Asn Ser Val Thr Gln Ser Asp
33                  35                  40                  45
34      agc gca agt aac gaa agc aaa agt aat gat tca agt agc gtt agt gct 492
35      Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser Ala
36              50                  55                  60
37      gca cct aaa aca gac gac aca aac gtg agt gat act aaa aca tcg tca 540
38      Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
39       65                  70                  75                  80
40      aac act aat aat ggc gaa acg agt gtg gcg caa aat cca gca caa cag 588
41      Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
42                      85                  90                  95
43      gaa acg aca caa tca tca tca aca aat gca act acg gaa gaa acg ccg 636
44      Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro
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46    gta act ggt gaa gct act act acg aca acg aat caa gct aat aca ccg   684
47    Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro
48             115                  120                 125
49    gca aca act caa tca agc aat aca aat gcg gag gaa tta gtg aat caa   732
50    Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln
51             130                  135                 140
52    aca agt aat gaa acg act ttt aat gat act aat aca gta tca tct gta   780
53    Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val
54    145                  150                  155                 160
55    aat tca cct caa aat tct aca aat gcg gaa aat gtt tca aca acg caa   828
56    Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
57                  165                  170                 175
58    gat act tca act gaa gca aca cct tca aac aat gaa tca gct cca cag   876
59    Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
60                  180                  185                 190
61    agt aca gat gca agt aat aaa gat gta gtt aat caa gcg gtt aat aca   924
62    Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
63             195                  200                 205
64    agt gcg cct aga atg aga gca ttt agt tta gcg gca gta gct gca gat   972
65    Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
66             210                  215                 220
67    gca ccg gca gct ggc aca gat att acg aat cag ttg acg aat gtg aca   1020
68    Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr
69    225                  230                  235                 240
70    gtt ggt att gac tct ggt acg act gtg tat ccg cac caa gca ggt tat   1068
71    Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr
72                  245                  250                 255
73    gtc aaa ctg aat tat ggt ttt tca gtg cct aat tct gct gtt aaa ggt   1116
74    Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly
75                  260                  265                 270
76    gac aca ttc aaa ata act gta cct aaa gaa tta aac tta aat ggt gta   1164
77    Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val
78             275                  280                 285
79    act tca act gct aaa gtg cca cca att atg gct gga gat caa gta ttg   1212
80    Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu
81             290                  295                 300
82    gca aat ggt gta atc gat agt gat ggt aat gtt att tat aca ttt aca   1260
83    Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr
84    305                  310                  315                 320
85    gac tat gta aat act aaa gat gat gta aaa gca act ttg acc atg ccc   1308
86    Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro
87                  325                  330                 335
88    gct tat att gac cct gaa aat gtt aaa aag aca ggt aat gtg aca ttg   1356
89    Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu
90                  340                  345                 350
91    gct act ggc ata ggt agt aca aca gca aac aaa aca gta tta gta gat   1404
92    Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val Asp
93             355                  360                 365
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 95       Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr Ile
 96          370                 375                 380
 97       gac caa atc gat aaa aca aat aat acg tat cgt cag aca att tat gtc    1500
 98       Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val
 99       385                 390                 395                 400
100        aat cca agt gga gat aac gtt att gcg ccg gtt tta aca ggt aat tta   1548
101       Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu
102                           405                 410                 415
103       aaa cca aat acg gat agt aat gca tta ata gat cag caa aat aca agt    1596
104       Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser
105                           420                 425                 430
106       att aaa gta tat aaa gta gat aat gca gct gat tta tct gaa agt tac    1644
107       Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr
108                           435                 440                 445
109       ttt gtg aat cca gaa aac ttt gag gat gtc act aat agt gtg aat att    1692
110       Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile
111          450                 455                 460
112       aca ttc cca aat cca aat caa tat aaa gta gag ttt aat acg cct gat    1740
113       Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp
114       465                 470                 475                 480
115       gat caa att aca aca ccg tat ata gta gtt gtt aat ggt cat att gat    1788
116       Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp
117                           485                 490                 495
118       ccg aat agc aaa ggt gat tta gct tta cgt tca act tta tat ggg tat    1836
119       Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr
120                           500                 505                 510
121       aac tcg aat ata att tgg cgc tct atg tca tgg gac aac gaa gta gca    1884
122       Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala
123                           515                 520                 525
124       ttt aat aac gga tca ggt tct ggt gac ggt atc gat aaa cca gtt gtt    1932
125       Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val
126          530                 535                 540
127       cct gaa caa cct gat gag cct ggt gaa att gaa cca att cca gag gat    1980
128       Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Asp
129       545                 550                 555                 560
130       tca gat tct gac cca ggt tca gat tct ggc agc gat tct aat tca gat    2028
131       Ser Asp Ser Asp Pro Gly Ser Asp Ser Gly Ser Asp Ser Asn Ser Asp
132                           565                 570                 575
133       agc ggt tca gat tcg ggt agt gat tct aca tca gat agt ggt tca gat    2076
134       Ser Gly Ser Asp Ser Gly Ser Asp Ser Thr Ser Asp Ser Gly Ser Asp
135                           580                 585                 590
136       tca gcg agt gat tca gat tca gca agt gat tca gac tca gcg agt gat    2124
137       Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp
138                595                 600                 605
139       tca gat tca gca agc gat tcc gac tca gcg agc gat tcc gac tca gac    2172
140       Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp
141          610                 615                 620
142       aat gac tcg gat tca gat agc gat tct gac tca gac agt gac tca gat    2220
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144      625                 630                 635                 640
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146      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
147                          645                 650                 655
148      tca gat tca gat agc gat tca gat tca gat agc gat tca gat tcc gac      2316
149      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
150                          660                 665                 670
151      agt gat tcc gac tca gac agc gat tct gac tcc gac agt gat tcc gac      2364
152      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
153                  675                 680                 685
154      tca gac agc gat tca gat tcc gac agt gat tcc gac tca gat agc gat      2412
155      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
156          690                 695                 700
157      tcc gac tca gat agc gac tca gat tca gac agc gat tca gat tca gac      2460
158      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
159      705                 710                 715                 720
160      agc gat tca gat tca gat agc gat tca gat tcc gac agt gac tca gat      2508
161      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
162                          725                 730                 735
163      tcc gac agt gac tcg gat tca gat agc gat tca gat tcc gac agt gac      2556
164      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
165                  740                 745                 750
166      tca gat tcc gac agt gac tca gac tca gac agt gat tcg gat tca gcg      2604
167      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala
168                  755                 760                 765
169      agt gat tcg gat tca gat agt gat tcc gac tcc gac agt gac tcg gat      2652
170      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
171          770                 775                 780
172      tca gat agc gac tca gac tcg gat agc gac tcg gat tca gat agc gat      2700
173      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
174      785                 790                 795                 800
175      tcg gac tca gat agc gat tca gaa tca gac agc gat tca gaa tca gac      2748
176      Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Glu Ser Asp
177                          805                 810                 815
178      agc gat tca gat tca gac agc gac tca gac agt gac tca gat tca gat      2796
179      Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
180                  820                 825                 830
181      agt gac tcg gat tca gcg agt gat tca gac tca ggt agt gac tcc gat      2844
182      Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp
183                  835                 840                 845
184      tca tca agt gat tcc gac tca gaa agt gat tca aat agc gat tcc gag      2892
185      Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser Asp Ser Glu
186          850                 855                 860
187      tca ggt tct aac aat aat gta gtt ccg cct aat tca cct aaa aat ggt      2940
188      Ser Gly Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro Lys Asn Gly
189      865                 870                 875                 880
190      act aat gct tct aat aaa aat gag gct aaa gat agt aaa gaa cca tta      2988
191      Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys Glu Pro Leu
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192                      885                   890                     .895
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195                      900                   905                     910
196       tta tta gca tca ata ggt tca tta cta ctt ttc aga aga aaa aaa gaa    3084
197       Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg Lys Lys Glu
198                      915                   920                     925
199       aat aaa gat aag aaa taagtaataa tgatattaaa ttaatcatat gattcatgaa    3139
200       Asn Lys Asp Lys Lys
201                      930
202       gaagccacct taaaaggtgc ttcttttact tggattttcc aaatatattg tttgaatata 3199
203       attaataatt aattcatcaa cagttaatta ttttaaaaag gtagatgtta tataatttgg 3259
204       cttggcgaaa aaatagggtg taaggtaggt tgttaattag ggaaaattaa ggagaaaata 3319
205       cagttgaaaa ataaattgct agttttatca ttgggagcat tatgtgtatc acaaatttgg 3379
206       gaaagtaatc gtgcgagtgc agtggtttct ggggagaaga atccatatgt atctgagtcg 3439
207       ttgaaactga ctaataataa aaataaatct agaacagtag aagagtataa gaaaagctt   3498
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210 <211> LENGTH: 933
211 <212> TYPE: PRT
212 <213> ORGANISM: Staphylococcus aureus
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217                      20                   25                  30
218       Ser Ser Lys Glu Ala Asp Ala Ser Glu Asn Ser Val Thr Gln Ser Asp
219                  35                   40                  45
220       Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser Ala
221              50                   55                  60
222       Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
223       65                   70                   75                  80
224       Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
225                      85                   90                  95
226       Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro
227                  100                  105                 110
228       Val Thr Gly Glu Ala Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro
229              115                  120                 125
230       Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln
231          130                  135                 140
232       Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val
233       145                  150                  155                 160
234       Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
235                  165                  170                 175
236       Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
237                  180                  185                 190
238       Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
239              195                  200                 205
240       Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
241          210                  215                 220
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